EDITORIAL
Cancer Discovery at One Year: The Editors’ Interim Analysis
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Jobs Wanted: Cancer Research
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RESEARCH WATCH
Selected highlights of recent articles of exceptional significance from the cancer literature

ONLINE
For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews.

RESEARCH BRIEFS
ATM Mutations in Patients with Hereditary Pancreatic Cancer
Précis: Next-generation sequencing identifies inherited ATM mutations in kindreds with hereditary pancreatic ductal adenocarcinoma.

Molecular Ontogeny of Donor-Derived Follicular Lymphomas Occurring after Hematopoietic Cell Transplantation
Précis: Analysis of a donor–recipient pair with follicular lymphoma reveals the time-course of somatic mutations acquired during lymphomagenesis.

Tackling Formalin-Fixed, Paraffin-Embedded Tissue with Next-Generation Sequencing
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Dissecting “PI3Kness”: The Complexity of Personalized Therapy for Ovarian Cancer
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The 14–3–3σ Tumor Suppressor Has Multiple Functions in ErbB2-Induced Breast Cancer
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Genomic Complexity and AKT Dependence in Serous Ovarian Cancer .................. 56

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High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing ......................... 82

Précis: Targeted, sequencing-based profiling of archival tumor samples identifies genetic alterations that can direct personalized therapy.

Loss of the 14–3–3σ Tumor Suppressor Is a Critical Event in ErbB2-Mediated Tumor Progression .................... 68
C. Ling, V-M-T. Su, D. Zu, and W.J. Muller


For more News and Research Watch, visit Cancer Discovery online at www.AACR.org/CDnews. Online-only News stories include the following:

• Biotech Firms Look for Virtual Success
• “Reversed” Krebs Cycle Can Feed Tumors
• Dual HER2 Blockade Slows Metastatic Breast Cancer
• Modified Stem Cells Create Tumor-Attacking T Cells

ON THE COVER

Wagle and colleagues describe a method to profile clinically relevant mutations in formalin-fixed, paraffin-embedded tumor samples involving exon capture of frequently mutated or polymorphic genes followed by massively parallel sequencing. This method identifies single-nucleotide variants, insertions, deletions, and copy number alterations overlooked by current genotyping-based methods with high specificity and sensitivity. Identification of such “actionable” genetic alterations that predict response to targeted or conventional cytotoxic therapies has the potential to facilitate individualized cancer treatment in a time- and cost-effective manner. For details, please see the article by Wagle and colleagues on page 82.